O'Bryen, Barbara

From: Switzer, Juliet
Sent: Thursday, October 14, 2004 2:10 PM
To: O'Bryen, Barbara
Subject: RE: alignment

sorry. seq id no 58 of serial number 10077176.
thanks.

-----Original Message-----
From: O'Bryen, Barbara
Sent: Thursday, October 14, 2004 2:10 PM
To: Switzer, Juliet
Subject: RE: alignment

It would be easier for me to do this if I had & seq id # & serial number.

-----Original Message-----
From: Switzer, Juliet
Sent: Thursday, October 14, 2004 2:02 PM
To: O'Bryen, Barbara
Subject: alignment

HI barb.
Will you please align nucleotides 252-1430 against GenBank X60012?
Will you let me know when you've done it- I'll come pick up the print out.
Thanks.
Juliet

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 16:31:10 ; Search time 1 Seconds
(without alignments)
2.780 Million cell updates/sec

Title: SEQ58-252-1430
Perfect score: 1179
Sequence: 1 atggaggagccgcagtcaga.....cagaagggcctgactcagac 1179

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 1179 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : x60012.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1179	100.0	1179	1	x60012	TOIG of: x60012
c 2	26.6	2.3	1179	1	x60012	TOIG of: x60012

ALIGNMENTS

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; LOCUS HSP53003 1179 bp mRNA linear PRI 23-JUN-1994
; DEFINITION Human mRNA for mutated p53 transformation suppressor gene.
; ACCESSION X60012
; VERSION X60012.1 GI:506436
; KEYWORDS p53 gene; p53 protein.
; SOURCE Homo sapiens (human)
; ORGANISM Homo sapiens
; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE 1 (bases 1 to 1179)
; AUTHORS Farrell,P.J., Allan,G.J., Shanahan,F., Vousden,K.H. and Crook,T.
; TITLE p53 is frequently mutated in Burkitt's lymphoma cell lines
; JOURNAL EMBO J. 10 (10), 2879-2887 (1991)
; MEDLINE 92007731
; PUBMED 1915267
; REFERENCE 2 (bases 1 to 1179)
; AUTHORS Farrell,P.J.
; TITLE Direct Submission
; JOURNAL Submitted (03-JUN-1991) P.J. Farrell, Ludwig Inst for Cancer Res,
; St Mary's Hospital Med School, Norfolk Place, London W2 1PG, UK
; COMMENT mutated p53 transformation suppressor gene.
; FEATURES Location/Qualifiers
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; /organism="Homo sapiens"
; /mol_type="mRNA"
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; D"
; ORIGIN
;
; X60012 Length: 1179 October 14, 2004 16:28 Type: N Check: 2359 ..
x60012

Query Match 100.0%; Score 1179; DB 1; Length 1179;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; LOCUS       HSP53003               1179 bp    mRNA    linear   PRI 23-JUN-1994
; DEFINITION  Human mRNA for mutated p53 transformation suppressor gene.
; ACCESSION   X60012
; VERSION     X60012.1  GI:506436
; KEYWORDS    p53 gene; p53 protein.
; SOURCE      Homo sapiens (human)
;   ORGANISM  Homo sapiens
;             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
;             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
; REFERENCE   1  (bases 1 to 1179)
;   AUTHORS   Farrell,P.J., Allan,G.J., Shanahan,F., Vousden,K.H. and Crook,T.
;   TITLE     p53 is frequently mutated in Burkitt's lymphoma cell lines
;   JOURNAL   EMBO J. 10 (10), 2879-2887 (1991)
;   MEDLINE   92007731
;    PUBMED   1915267
; REFERENCE   2  (bases 1 to 1179)
;   AUTHORS   Farrell,P.J.
;   TITLE     Direct Submission
;   JOURNAL   Submitted (03-JUN-1991) P.J. Farrell, Ludwig Inst for Cancer Res,
;             St Mary's Hospital Med School, Norfolk Place, London W2 1PG, UK
; COMMENT     mutated p53 transformation suppressor gene.
; FEATURES             Location/Qualifiers
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;                      D"
; ORIGIN
;
;  X60012  Length: 1179  October 14, 2004 16:28  Type: N  Check: 2359  ..
x60012

  Query Match             2.3%;  Score 26.6;  DB 1;  Length 1179;
  Best Local Similarity   51.2%;  Pred. No. 0;
  Matches   62;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

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Qy        294 T 294
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Db        174 T 174


Search completed: October 14, 2004, 16:31:11
Job time : 1 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 28, 2004, 12:05:54 ; Search time 16 Seconds
(without alignments)
2.637 Million cell updates/sec

Title: SEQ58-252-1430
Perfect score: 1179
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 13 seqs, 17894 residues

Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : issdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1179	100.0	1182	1	US-08-184-009-215	Sequence 215, App
	2	1179	100.0	1182	1	US-08-458-356-215	Sequence 215, App
	3	1179	100.0	1182	1	US-08-796-101-46	Sequence 46, Appl
	4	1179	100.0	1182	1	US-08-460-736-215	Sequence 215, App
	5	1179	100.0	1182	1	US-09-535-370-215	Sequence 215, App
	6	1179	100.0	1484	1	US-08-184-009-103	Sequence 103, App
	7	1179	100.0	1484	1	US-08-458-356-103	Sequence 103, App
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	9	1179	100.0	1484	1	US-09-535-370-103	Sequence 103, App
	10	1179	100.0	1512	1	US-08-184-009-99	Sequence 99, Appl
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c	20	26.6	2.3	1484	1	US-08-458-356-103	Sequence 103, App
c	21	26.6	2.3	1484	1	US-08-460-736-103	Sequence 103, App
c	22	26.6	2.3	1484	1	US-09-535-370-103	Sequence 103, App
c	23	26.6	2.3	1512	1	US-08-184-009-99	Sequence 99, Appl
c	24	26.6	2.3	1512	1	US-08-458-356-99	Sequence 99, Appl
c	25	26.6	2.3	1512	1	US-08-460-736-99	Sequence 99, Appl
c	26	26.6	2.3	1512	1	US-09-535-370-99	Sequence 99, Appl

ALIGNMENTS

RESULT 1
US-08-184-009-215

; Sequence 215, Application US/08184009
; Patent No. 5833975
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I.
; TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 217
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,009
; FILING DATE: 19-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELEX: 425066CURTMS
; INFORMATION FOR SEQ ID NO: 215:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1182 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-184-009-215

Query Match 100.0%; Score 1179; DB 1; Length 1182;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 1179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
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Db        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180

Qy        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
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Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
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Qy        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
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Db        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960

Qy        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020

Qy       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080

Qy       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140

Qy       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
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Db       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
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RESULT 2
US-08-458-356-215
; Sequence 215, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  215:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1182 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-458-356-215

  Query Match             100.0%;  Score 1179;  DB 1;  Length 1182;
  Best Local Similarity   100.0%;  Pred. No. 0.00062;
  Matches 1179;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60

Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
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Db         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120

Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180

Qy        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240

Qy        241 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300

Qy        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360

Qy        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420

Qy        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480

Qy        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540

Qy        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
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Db        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600

Qy        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
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Qy        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
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Db        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720

Qy        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780

Qy        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840

Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
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Db        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900

Qy        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960

Qy        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020

Qy       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
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Db       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080

Qy       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
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Db       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140

Qy       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
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Db       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
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RESULT 3
US-08-796-101-46
; Sequence 46, Application US/08796101
; Patent No. 6183752
;  GENERAL INFORMATION:
;    APPLICANT:  EPSTEIN, STEPHEN E.
;    APPLICANT:  FINKEL, TOREN
;    APPLICANT:  SPEIR, EDITH
;    APPLICANT:  ZHOU, YI FU
;    APPLICANT:  ZHU, JIANHUI
;    APPLICANT:  ERDILE, LORNE
;    APPLICANT:  PINCUS, STEVEN
;    TITLE OF INVENTION:  RESTENOSIS/ATHEROSCLEROSIS DIAGNOSIS,
;    TITLE OF INVENTION:  PROPHYLAXIS AND THERAPY
;    NUMBER OF SEQUENCES:  184
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CURTIS, MORRIS & SAFFORD, P.C.
;      STREET:  530 FIFTH AVENUE
;      CITY:  NEW YORK
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/796,101
;      FILING DATE:  05-FEB-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KOWALSKI, THOMAS J.
;      REGISTRATION NUMBER:  32,147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 764-5574
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1182 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-796-101-46

  Query Match           100.0%;  Score 1179;  DB 1;  Length 1182;
  Best Local Similarity  100.0%;  Pred. No. 0.00062;
  Matches 1179;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
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Db          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60

Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
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Db         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120

Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180

Qy        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
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Db        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240

Qy        241 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
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Db        241 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300

Qy        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
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Db        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360

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Qy        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
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Qy        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
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Db        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540

Qy        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
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Db        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600

Qy        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
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Db        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660

Qy        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720

Qy        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780

Qy        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840

Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900

Qy        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960

Qy        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020

Qy       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
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Db       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080

Qy       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
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Db       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140

Qy       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
              |||||||||||||||||||||||||||||||||||||||
Db       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179


RESULT 4
US-08-460-736-215
; Sequence 215, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  215:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1182 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-215

  Query Match             100.0%;  Score 1179;  DB 1;  Length 1182;
  Best Local Similarity   100.0%;  Pred. No. 0.00062;
  Matches 1179;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
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Db          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60

Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
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Db         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120

Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
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Db        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180

Qy        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
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Db        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240

Qy        241 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCCTGTCATCTTCTGTCCCTTCCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCCTGTCATCTTCTGTCCCTTCCCAG 300

Qy        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
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Db        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360

Qy        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
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Db        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420

Qy        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
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Qy        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
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Db        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540

Qy        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600

Qy        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660

Qy        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720

Qy        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
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Db        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780

Qy        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840

Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
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Db        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900

Qy        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960

Qy        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020

Qy       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080

Qy       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
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Db       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140

Qy       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
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Db       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179

RESULT 5
US-09-535-370-215
; Sequence 215, Application US/09535370
; Patent No. 6537594
;  GENERAL INFORMATION:
;       APPLICANT: Paoletti, Enzo
;                  Tartaglia, James
;                  Cox, William I.
;       TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;       NUMBER OF SEQUENCES: 217
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Curtis, Morris & Safford
;            STREET: 530 Fifth Avenue
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: 10036
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/535,370
;            FILING DATE: 24-Mar-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/460,736
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Frommer, William S.
;            REGISTRATION NUMBER: 25,506
;            REFERENCE/DOCKET NUMBER: 454310-2530
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212) 840-3333
;            TELEFAX: (212) 840-0712
;            TELEX: 425066CURTMS
;  INFORMATION FOR SEQ ID NO: 215:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1182 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-09-535-370-215

  Query Match             100.0%;  Score 1179;  DB 1;  Length 1182;
  Best Local Similarity   100.0%;  Pred. No. 0.00062;
  Matches 1179;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60

Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120

Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180

Qy        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240

Qy        241 ACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300

Qy        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360

Qy        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420

Qy        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480

Qy        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540

Qy        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600

Qy        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660

Qy        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720

Qy        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780

Qy        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840

Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900

Qy        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960

Qy        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020

Qy       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080

Qy       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140

Qy       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
              |||||||||||||||||||||||||||||||||||||||
Db       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179

RESULT 6
US-08-184-009-103
; Sequence 103, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
```

```
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  103:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1484 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-103

  Query Match             100.0%;  Score 1179;  DB 1;  Length 1484;
  Best Local Similarity   100.0%;  Pred. No. 0.00049;
  Matches 1179;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 292

Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 352

Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 412

Qy        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 472

Qy        241 ACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 ACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 532

Qy        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 592

Qy        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 652

Qy        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 712

Qy        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 772

Qy        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 832

Qy        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 892

Qy        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 952

Qy        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        953 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 1012

Qy        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1013 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 1072

Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1073 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 1132

Qy        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
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Db       1133 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 1192

Qy        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
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Db       1193 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1252

Qy       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1253 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1312

Qy       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1313 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1372

Qy       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
              ||||||||||||||||||||||||||||||||||||||||
Db       1373 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1411


RESULT 7
US-08-458-356-103
; Sequence 103, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
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;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  103:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1484 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-458-356-103

  Query Match           100.0%;  Score 1179;  DB 1;  Length 1484;
  Best Local Similarity  100.0%;  Pred. No. 0.00049;
  Matches 1179;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 292

Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 352

Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 412

Qy        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 472

Qy        241 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 ACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 532

Qy        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 592

Qy        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 652

Qy        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 712

Qy        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 772

Qy        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 832

Qy        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 892

Qy        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 952

Qy        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        953 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 1012

Qy        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1013 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 1072

Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1073 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 1132

Qy        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1133 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 1192

Qy        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1193 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1252

Qy       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1253 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1312

Qy       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1313 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1372

Qy       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
              ||||||||||||||||||||||||||||||||||||||||
Db       1373 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1411


RESULT 8
US-08-460-736-103
; Sequence 103, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  103:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  1484 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-103

  Query Match             100.0%;  Score 1179;  DB 1;  Length 1484;
  Best Local Similarity   100.0%;  Pred. No. 0.00049;
  Matches 1179;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 292

Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        293 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 352

Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        353 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 412

Qy        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 472

Qy        241 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 532

Qy        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        533 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 592

Qy        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 652

Qy        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        653 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 712

Qy        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        713 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 772

Qy        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        773 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 832

Qy        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        833 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 892

Qy        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        893 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 952

Qy        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        953 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 1012

Qy        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1013 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 1072

Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1073 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 1132

Qy        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1133 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 1192

Qy        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1193 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1252

Qy       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1253 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1312

Qy       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1313 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1372

Qy       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
              |||||||||||||||||||||||||||||||||||||||
Db       1373 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1411


RESULT 9
US-09-535-370-103
; Sequence 103, Application US/09535370
; Patent No. 6537594
;   GENERAL INFORMATION:
;        APPLICANT: Paoletti, Enzo
;                   Tartaglia, James
;                   Cox, William I.
;        TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;        NUMBER OF SEQUENCES: 217
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Curtis, Morris & Safford
;             STREET: 530 Fifth Avenue
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/535,370
;             FILING DATE: 24-Mar-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/460,736
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Frommer, William S.
;             REGISTRATION NUMBER: 25,506
;             REFERENCE/DOCKET NUMBER: 454310-2530
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 840-3333
;             TELEFAX: (212) 840-0712
;             TELEX: 425066CURTMS
;   INFORMATION FOR SEQ ID NO: 103:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1484 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-09-535-370-103

  Query Match             100.0%;  Score 1179;  DB 1;  Length 1484;
  Best Local Similarity   100.0%;  Pred. No. 0.00049;
  Matches 1179;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 292
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Qy        61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
Db       293 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 352

Qy       121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
Db       353 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 412

Qy       181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
Db       413 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 472

Qy       241 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
Db       473 ACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 532

Qy       301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
Db       533 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 592

Qy       361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
Db       593 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 652

Qy       421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
Db       653 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 712

Qy       481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
Db       713 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 772

Qy       541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
Db       773 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 832

Qy       601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
Db       833 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 892

Qy       661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
Db       893 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 952

Qy       721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
Db       953 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 1012

Qy       781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
Db      1013 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 1072

Qy       841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
Db      1073 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 1132

Qy       901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
Db      1133 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 1192

Qy       961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
Db      1193 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1252

Qy      1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
Db      1253 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1312

Qy      1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
Db      1313 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1372

Qy      1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
Db      1373 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1411
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RESULT 10
US-08-184-009-99
; Sequence 99, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  99:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1512 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-99

  Query Match           100.0%;  Score 1179;  DB 1;  Length 1512;
  Best Local Similarity  100.0%;  Pred. No. 0.00048;
  Matches 1179;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
Db        269 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 328

Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
Db        329 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 388

Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
Db        389 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 448

Qy        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
Db        449 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 508

Qy        241 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
Db        509 ACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 568

Qy        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
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Db        569 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 628

Qy        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        629 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 688

Qy        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        689 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 748

Qy        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        749 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 808

Qy        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        809 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 868

Qy        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        869 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 928

Qy        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        929 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 988

Qy        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        989 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 1048

Qy        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1049 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 1108

Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1109 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 1168

Qy        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1169 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 1228

Qy        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1229 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1288

Qy       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1289 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1348

Qy       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1349 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1408

Qy       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
              ||||||||||||||||||||||||||||||||||||||||
Db       1409 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1447
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RESULT 11
US-08-458-356-99
; Sequence 99, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  99:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1512 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-458-356-99

  Query Match           100.0%;  Score 1179;  DB 1;  Length 1512;
  Best Local Similarity  100.0%;  Pred. No. 0.00048;
  Matches 1179;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 328

Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 388

Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 448

Qy        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 508

Qy        241 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 568

Qy        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        569 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 628

Qy        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        629 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 688

Qy        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        689 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 748

Qy        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        749 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 808
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Qy        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        809 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 868

Qy        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        869 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 928

Qy        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        929 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 988

Qy        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        989 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 1048

Qy        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1049 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 1108

Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1109 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 1168

Qy        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1169 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 1228

Qy        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1229 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1288

Qy       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1289 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1348

Qy       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1349 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1408

Qy       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
              |||||||||||||||||||||||||||||||||||||||
Db       1409 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1447
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RESULT 12
US-08-460-736-99
; Sequence 99, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  99:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1512 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-99

  Query Match             100.0%;  Score 1179;  DB 1;  Length 1512;
  Best Local Similarity   100.0%;  Pred. No. 0.00048;
  Matches 1179;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
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Db        269 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 328

Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 388

Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 448

Qy        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
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Db        449 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 508

Qy        241 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
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Db        509 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 568

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Db        569 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 628

Qy        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
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Qy        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        689 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 748

Qy        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        749 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 808

Qy        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
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Db        869 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 928

Qy        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
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Db        929 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 988

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Db        989 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 1048
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Qy        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1049 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 1108

Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1109 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 1168

Qy        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1169 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 1228

Qy        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
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Qy       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
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Qy       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
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Db       1349 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1408

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Db       1409 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1447
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RESULT 13
US-09-535-370-99
; Sequence 99, Application US/09535370
; Patent No. 6537594
;   GENERAL INFORMATION:
;        APPLICANT: Paoletti, Enzo
;                   Tartaglia, James
;                   Cox, William I.
;        TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
;        NUMBER OF SEQUENCES: 217
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Curtis, Morris & Safford
;             STREET: 530 Fifth Avenue
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/535,370
;             FILING DATE: 24-Mar-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/460,736
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Frommer, William S.
;             REGISTRATION NUMBER: 25,506
;             REFERENCE/DOCKET NUMBER: 454310-2530
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 840-3333
;             TELEFAX: (212) 840-0712
;             TELEX: 425066CURTMS
;   INFORMATION FOR SEQ ID NO: 99:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1512 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-09-535-370-99

  Query Match           100.0%;  Score 1179;  DB 1;  Length 1512;
  Best Local Similarity  100.0%;  Pred. No. 0.00048;
  Matches 1179;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 328

Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
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Db        329 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 388

Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 448

Qy        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
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Db        449 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 508

Qy        241 ACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
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Db        509 ACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 568

Qy        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
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Db        569 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 628

Qy        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        629 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 688

Qy        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        689 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 748

Qy        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
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Db        749 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 808

Qy        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
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Db        809 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 868

Qy        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        869 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 928

Qy        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
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Db        929 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 988

Qy        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
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Db        989 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 1048

Qy        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1049 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 1108

Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1109 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 1168

Qy        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
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Db       1169 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 1228

Qy        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
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Db       1229 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1288

Qy       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1289 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1348

Qy       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1349 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1408

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Db       1409 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1447


RESULT 14
US-08-184-009-215/c
; Sequence 215, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  215:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1182 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-215

  Query Match             2.3%;  Score 26.6;  DB 1;  Length 1182;
  Best Local Similarity   51.2%;  Pred. No. 13;
  Matches   62;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

Qy       174 AGGTCCAGATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGC 233
                 |||  |||| || |       |   | |||||  | |  | |  |||  || |  |||
Db       294 AGGGACAGAAGATGACAGGGGCCAGGAGGGGGCTGGTGCAGGGGCCGCCGGTGTAGGAGC 235

Qy       234 AGCTCCTACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCC 293
                 |||  | ||  |||  | |  | | |||||  |    |      | || ||||  ||
Db       234 TGCTGGTGCAGGGGCCACGCGGGGAGCAGCCTCTGGCATTCTGGGAGCTTCATCTGGACC 175

Qy       294 T 294
                 |
Db       174 T 174


RESULT 15
US-08-458-356-215/c
; Sequence 215, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  215:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1182 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-458-356-215

  Query Match             2.3%;  Score 26.6;  DB 1;  Length 1182;
  Best Local Similarity   51.2%;  Pred. No. 13;
  Matches   62;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

Qy       174 AGGTCCAGATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGC 233
                 |||  |||| || |       |   | |||||  | |  | |  |||  || |  |||
Db       294 AGGGACAGAAGATGACAGGGGCCAGGAGGGGGCTGGTGCAGGGGCCGCCGGTGTAGGAGC 235

Qy       234 AGCTCCTACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCC 293
                 |||  | ||  |||  | |  | | |||||  |    |      | || ||||  ||
Db       234 TGCTGGTGCAGGGGCCACGCGGGGAGCAGCCTCTGGCATTCTGGGAGCTTCATCTGGACC 175

Qy       294 T 294
                 |
Db       174 T 174


Search completed: September 28, 2004, 12:06:14
Job time : 20 secs
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OM nucleic - nucleic search, using sw model

Run on: September 28, 2004, 12:07:16 ; Search time 15 Seconds
(without alignments)
2.663 Million cell updates/sec

Title: SEQ58-252-1430
Perfect score: 1179
Sequence: 1 atggaggagccgcagtcaga.....cagaagggcctgactcagac 1179

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 10 seqs, 16943 residues

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : ngsdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1179	100.0	1182	1	AAQ67884	Human p53 DNA. Sy
	2	1179	100.0	1182	1	AAZ08529	Human p53 gene. H
	3	1179	100.0	1182	1	AAH19387	p53 coding sequenc
	4	1179	100.0	1484	1	AAZ08435	H6/p53 (wildtype)
	5	1179	100.0	1512	1	AAZ08434	H6/p53 (wildtype)
	6	1179	100.0	2061	1	ADD93292	p53-Chk1(1-270) fu
	7	1179	100.0	2367	1	ADD93290	p53-SGK(60-431) fu
	8	1179	100.0	2385	1	ADD93288	p53-Myt1(1-378) fu
	9	1179	100.0	2406	1	ADD93286	p53-Yak3 fusion pr
	10	1177.4	99.9	1182	1	ADC35154	Human breast cance
c	11	26.6	2.3	1182	1	AAQ67884	Human p53 DNA. Sy
c	12	26.6	2.3	1182	1	AAZ08529	Human p53 gene. H
c	13	26.6	2.3	1182	1	AAH19387	p53 coding sequenc
c	14	26.6	2.3	1182	1	ADC35154	Human breast cance
c	15	26.6	2.3	1484	1	AAZ08435	H6/p53 (wildtype)
c	16	26.6	2.3	1512	1	AAZ08434	H6/p53 (wildtype)
c	17	26.6	2.3	2061	1	ADD93292	p53-Chk1(1-270) fu
c	18	26.6	2.3	2367	1	ADD93290	p53-SGK(60-431) fu
c	19	26.6	2.3	2385	1	ADD93288	p53-Myt1(1-378) fu
c	20	26.6	2.3	2406	1	ADD93286	p53-Yak3 fusion pr

ALIGNMENTS

RESULT 1
AAQ67884
ID AAQ67884 standard; DNA; 1182 BP.
XX
AC AAQ67884;
XX
DT 25-MAR-2003 (revised)
DT 23-MAR-1995 (first entry)
XX
DE Human p53 DNA.
XX
KW Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
KW murine; interleukin-2; IL-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector;
KW plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response;
KW polymerase chain reaction; poxvirus; pSD542; immunological response;
KW pathogen; human; interferon; IFN; ss.
XX
OS Synthetic.
XX
PN WO9416716-A1.
XX
PD 04-AUG-1994.
XX
PF 21-JAN-1994; 94WO-US000888.
XX
PR 21-JAN-1993; 93US-00007115.
PR 19-JAN-1994; 94US-00184009.
XX
PA (VIRO-) VIROGENETICS CORP.
XX
PI Paoletti E, Tartaglia J, Cox WI;
XX
DR WPI; 1994-263767/32.
XX
PT Attenuated recombinant virus used for cancer therapy - comprises DNA
PT encoding cytokine and/or tumour associated antigen.
XX
PS Example 32; Fig 39; 232pp; English.
XX
CC This sequence represents the wildtype human p53 gene from the translation
CC initiation codon to the stop codon. This sequence was used in the
CC construction of an ALVAC-based recombinant virus containing a mutant form
CC of the human p53 gene. The mutant form has a G>A substitution at position
CC 524, changing an Arg residue at position 175 to a His residue. The
CC plasmid pMM110 (see also AAQ67864) contains the vaccinia H6 promoter and
CC the wild type human p53 gene in the ALVAC C5 insertion site. The mutant
CC p53 gene was obtained from plasmid Cx22A and cloned into pMM110 to
CC generate pMM143. Recombination between pMM143 and ALVAC rescuing virus
CC produced recombinant virus vCP270, which contains the vaccinia H6
CC promoted mutated human p53 in the C5 locus. The resulting virus may be
CC used in a composition for inducing an antigenic or immunological
CC response, ie. for immunisation against pathogens. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 1182 BP; 276 A; 365 C; 307 G; 234 T; 0 U; 0 Other;

Query Match 100.0%; Score 1179; DB 1; Length 1182;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 1179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60

Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120

Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180

Qy        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240

Qy        241 ACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300

Qy        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360

Qy        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420

Qy        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480

Qy        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540

Qy        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600

Qy        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660

Qy        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720

Qy        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780

Qy        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840

Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900

Qy        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960

Qy        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020

Qy       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080

Qy       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140

Qy       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
              |||||||||||||||||||||||||||||||||||||||
Db       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
```

RESULT 2
AAZ08529
ID AAZ08529 standard; DNA; 1182 BP.
XX
AC AAZ08529;
XX
DT 19-OCT-1999 (first entry)
XX
DE Human p53 gene.
XX
KW Attenuated recombinant virus; cytokine; tumour associated antigen;
KW NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rabies;
KW cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF;
KW interleukin; interferon; IFN-gamma; IL-4; melanoma associated antigen;
KW carcinoembryonic antigen; immunisation; antigenic; poxvirus; influenza;
KW immunological response; immunotherapy; vaccine; Newcastle Disease; ss.
XX
OS Homo sapiens.
XX
PN US5942235-A.
XX
PD 24-AUG-1999.
XX
PF 02-JUN-1995; 95US-00458356.
XX
PR 24-DEC-1981; 81US-00334456.
PR 08-DEC-1982; 82US-00446824.
PR 19-JUN-1984; 84US-00622135.
PR 27-AUG-1987; 87US-00090209.
PR 28-AUG-1987; 87US-00090711.
PR 20-OCT-1987; 87US-00110335.
PR 25-APR-1988; 88US-00186054.
PR 23-AUG-1988; 88US-00234390.
PR 14-JUN-1990; 90US-00537882.
PR 14-JUN-1990; 90US-00537890.
PR 16-DEC-1991; 91US-00805567.
PR 03-MAR-1992; 92US-00847977.
PR 06-MAR-1992; 92US-00847951.
PR 04-MAY-1992; 92US-00881995.
PR 22-JUL-1992; 92US-00918278.
PR 20-JAN-1993; 93US-00007115.
PR 19-JAN-1994; 94US-00184009.
PR 14-APR-1994; 94US-00228926.
PR 13-SEP-1994; 94US-00306259.
XX
PA (HEAL-) HEALTH RES INC.
XX
PI Paoletti E;
XX
DR WPI; 1999-493494/41.
XX
PT Recombinant poxviruses comprising exogenous DNA encoding antigenic
PT determinants useful in immunotherapy to immunize against cancers and
PT other diseases such as influenza, Newcastle Disease and rabies.
XX
PS Example 32; Fig 39; 163pp; English.
XX
CC The present invention describes a recombinant poxvirus (I), comprising
CC exogenous DNA encoding an antigenic determinant of a pathogen which is
CC then expressed in vivo in infected host cells after administration to a
CC patient and therefore induces an immunological response. (I) may be used
CC to vaccinate patients against a wide range of diseases and disorders
CC depending on the type of antigen encoded by the exogenous DNA. (I) may be
CC used to vaccinate against diseases such as rabies, influenza and
CC Newcastle Disease. It is particularly useful for immunising against
CC cancers. The poxvirus (I) also provides a means of manipulating
CC lymphocytes and tumour cells for use in cell-based immunotherapeutic
CC modalities for cancer. (I) also have enhanced safety compared to
CC unattenuated viruses (attenuation reduces the virulence of the viruses)
CC and known recombinant poxvirus vaccines. This increased level of safety
CC reduces the possibility of a 'runaway' infection in the host and reduces
CC the chance of transmission from vaccinated to unvaccinated individuals
CC and contamination of the environment. The present sequence represents a
CC human p53 gene used in the exemplification of the present invention
XX
SQ Sequence 1182 BP; 276 A; 365 C; 307 G; 234 T; 0 U; 0 Other;

Query Match 100.0%; Score 1179; DB 1; Length 1182;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 1179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60

Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
```

```
Db        61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
Qy       121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
Db       121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
Qy       181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
Db       181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
Qy       241 ACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
Db       241 ACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
Qy       301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
Db       301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
Qy       361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
Db       361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
Qy       421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
Db       421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
Qy       481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
Db       481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
Qy       541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
Db       541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
Qy       601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
Db       601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
Qy       661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
Db       661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
Qy       721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
Db       721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
Qy       781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
Db       781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
Qy       841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
Db       841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
Qy       901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
Db       901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
Qy       961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
Db       961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
Qy      1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
Db      1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
Qy      1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
Db      1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
Qy      1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
Db      1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
```

RESULT 3
AAH19387
ID AAH19387 standard; cDNA; 1182 BP.
XX
AC AAH19387;
XX
DT 03-AUG-2001 (first entry)
XX
DE p53 coding sequence.
XX
KW Cytostatic; gene therapy; p53; tumour; ss.
XX
OS Unidentified.
XX
PN JP2000354488-A.
XX
PD 26-DEC-2000.
XX
PF 09-APR-1999; 99JP-00139034.
XX
PR 09-APR-1999; 99JP-00139034.
XX
PA (IKAW/) IKAWA H.
PA (SAKA) OTSUKA PHARM CO LTD.
XX
DR WPI; 2001-268293/28.
DR P-PSDB; AAB84836.
XX
PT Chimera gene of the p53 family, useful for gene therapy, and treatment of
PT cancer, comprises a transcription activating region and a DNA binding
PT region.
XX
PS Disclosure; Fig 2; 57pp; Japanese.
XX
CC The present invention relates to a chimera gene of p53 family encoding a
CC transcription activating region, a DNA binding region, and an oligomer
CC formation region of different p53 family proteins. The chimeric gene can
CC be used for gene therapy of p53 variant human tumours, and analysis of
CC the function of the p53 family gene. The present sequence was used in the
CC present invention
XX
SQ Sequence 1182 BP; 276 A; 365 C; 307 G; 234 T; 0 U; 0 Other;

Query Match 100.0%; Score 1179; DB 1; Length 1182;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 1179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
Db          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
Db         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
Db        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
Qy        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
Db        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
Qy        241 ACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
Db        241 ACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
Qy        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
Db        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
```

```
Qy        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420

Qy        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480

Qy        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540

Qy        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600

Qy        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660

Qy        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720

Qy        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780

Qy        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840

Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900

Qy        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960

Qy        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020

Qy       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080

Qy       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140

Qy       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
              |||||||||||||||||||||||||||||||||||||||
Db       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
```

RESULT 4
AAZ08435
ID AAZ08435 standard; DNA; 1484 BP.
XX
AC AAZ08435;
XX
DT 19-OCT-1999 (first entry)
XX
DE H6/p53 (wildtype) expression cassette and flanking regions from vCP207.
XX
KW Attenuated recombinant virus; cytokine; tumour associated antigen;
KW NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rabies;
KW cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF;
KW interleukin; interferon; IFN-gamma; IL-4; melanoma associated antigen;
KW carcinoembryonic antigen; immunisation; antigenic; poxvirus; influenza;
KW immunological response; immunotherapy; vaccine; Newcastle Disease; ss.
XX
OS Synthetic.
OS Homo sapiens.
OS Vaccinia virus.
XX
PN US5942235-A.
XX
PD 24-AUG-1999.
XX
PF 02-JUN-1995; 95US-00458356.
XX
PR 24-DEC-1981; 81US-00334456.
PR 08-DEC-1982; 82US-00446824.
PR 19-JUN-1984; 84US-00622135.
PR 27-AUG-1987; 87US-00090209.
PR 28-AUG-1987; 87US-00090711.
PR 20-OCT-1987; 87US-00110335.
PR 25-APR-1988; 88US-00186054.
PR 23-AUG-1988; 88US-00234390.
PR 14-JUN-1990; 90US-00537882.
PR 14-JUN-1990; 90US-00537890.
PR 16-DEC-1991; 91US-00805567.
PR 03-MAR-1992; 92US-00847977.
PR 06-MAR-1992; 92US-00847951.
PR 04-MAY-1992; 92US-00881995.
PR 22-JUL-1992; 92US-00918278.
PR 20-JAN-1993; 93US-00007115.
PR 19-JAN-1994; 94US-00184009.
PR 14-APR-1994; 94US-00228926.
PR 13-SEP-1994; 94US-00306259.
XX
PA (HEAL-) HEALTH RES INC.
XX
PI Paoletti E;
XX
DR WPI; 1999-493494/41.
XX
PT Recombinant poxviruses comprising exogenous DNA encoding antigenic
PT determinants useful in immunotherapy to immunize against cancers and
PT other diseases such as influenza, Newcastle Disease and rabies.
XX
PS Example 15; Fig 18; 163pp; English.
XX
CC The present invention describes a recombinant poxvirus (I), comprising
CC exogenous DNA encoding an antigenic determinant of a pathogen which is
CC then expressed in vivo in infected host cells after administration to a
CC patient and therefore induces an immunological response. (I) may be used
CC to vaccinate patients against a wide range of diseases and disorders
CC depending on the type of antigen encoded by the exogenous DNA. (I) may be
CC used to vaccinate against diseases such as rabies, influenza and
CC Newcastle Disease. It is particularly useful for immunising against
CC cancers. The poxvirus (I) also provides a means of manipulating
CC lymphocytes and tumour cells for use in cell-based immunotherapeutic
CC modalities for cancer. (I) also have enhanced safety compared to
CC unattenuated viruses (attenuation reduces the virulence of the viruses)
CC and known recombinant poxvirus vaccines. This increased level of safety
CC reduces the possibility of a 'runaway' infection in the host and reduces
CC the chance of transmission from vaccinated to unvaccinated individuals
CC and contamination of the environment. The present sequence represents a
CC H6/p53 (wildtype) expression cassette and flanking regions from vCP207
CC used in the exemplification of the present invention
XX
SQ Sequence 1484 BP; 367 A; 416 C; 371 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 1179; DB 1; Length 1484;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 1179; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        233 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 292
```

```
Qy        61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       293 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 352

Qy       121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       353 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 412

Qy       181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       413 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 472

Qy       241 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       473 ACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 532

Qy       301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       533 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 592

Qy       361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       593 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 652

Qy       421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       653 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 712

Qy       481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       713 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 772

Qy       541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       773 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 832

Qy       601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       833 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 892

Qy       661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       893 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 952

Qy       721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       953 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 1012

Qy       781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1013 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 1072

Qy       841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1073 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 1132

Qy       901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1133 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 1192

Qy       961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1193 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1252

Qy      1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1253 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1312

Qy      1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1313 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1372

Qy      1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
             |||||||||||||||||||||||||||||||||||||||
Db      1373 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1411
```

RESULT 5
AAZ08434
ID AAZ08434 standard; DNA; 1512 BP.
XX
AC AAZ08434;
XX
DT 19-OCT-1999 (first entry)
XX
DE H6/p53 (wildtype) expression cassette and flanking regions from vP1101.
XX
KW Attenuated recombinant virus; cytokine; tumour associated antigen;
KW NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rabies;
KW cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF;
KW interleukin; interferon; IFN-gamma; IL-4; melanoma associated antigen;
KW carcinoembryonic antigen; immunisation; antigenic; poxvirus; influenza;
KW immunological response; immunotherapy; vaccine; Newcastle Disease; ss.
XX
OS Synthetic.
OS Homo sapiens.
OS Vaccinia virus.
XX
PN US5942235-A.
XX
PD 24-AUG-1999.
XX
PF 02-JUN-1995; 95US-00458356.
XX
PR 24-DEC-1981; 81US-00334456.
PR 08-DEC-1982; 82US-00446824.
PR 19-JUN-1984; 84US-00622135.
PR 27-AUG-1987; 87US-00090209.
PR 28-AUG-1987; 87US-00090711.
PR 20-OCT-1987; 87US-00110335.
PR 25-APR-1988; 88US-00186054.
PR 23-AUG-1988; 88US-00234390.
PR 14-JUN-1990; 90US-00537882.
PR 14-JUN-1990; 90US-00537890.
PR 16-DEC-1991; 91US-00805567.
PR 03-MAR-1992; 92US-00847977.
PR 06-MAR-1992; 92US-00847951.
PR 04-MAY-1992; 92US-00881995.
PR 22-JUL-1992; 92US-00918278.
PR 20-JAN-1993; 93US-00007115.
PR 19-JAN-1994; 94US-00184009.
PR 14-APR-1994; 94US-00228926.
PR 13-SEP-1994; 94US-00306259.
XX
PA (HEAL-) HEALTH RES INC.
XX
PI Paoletti E;
XX
DR WPI; 1999-493494/41.
XX
PT Recombinant poxviruses comprising exogenous DNA encoding antigenic
PT determinants useful in immunotherapy to immunize against cancers and
PT other diseases such as influenza, Newcastle Disease and rabies.
XX
PS Example 15; Fig 17; 163pp; English.
XX
CC The present invention describes a recombinant poxvirus (I), comprising
CC exogenous DNA encoding an antigenic determinant of a pathogen which is
CC then expressed in vivo in infected host cells after administration to a
CC patient and therefore induces an immunological response. (I) may be used
CC to vaccinate patients against a wide range of diseases and disorders
CC depending on the type of antigen encoded by the exogenous DNA. (I) may be
CC used to vaccinate against diseases such as rabies, influenza and
CC Newcastle Disease. It is particularly useful for immunising against
CC cancers. The poxvirus (I) also provides a means of manipulating
CC lymphocytes and tumour cells for use in cell-based immunotherapeutic

```
CC   modalities for cancer. (I) also have enhanced safety compared to
CC   unattenuated viruses (attenuation reduces the virulence of the viruses)
CC   and known recombinant poxvirus vaccines. This increased level of safety
CC   reduces the possibility of a 'runaway' infection in the host and reduces
CC   the chance of transmission from vaccinated to unvaccinated individuals
CC   and contamination of the environment. The present sequence represents a
CC   H6/p53 (wildtype) expression cassette and flanking regions from vP1101
CC   used in the exemplification of the present invention
XX
SQ   Sequence 1512 BP; 379 A; 420 C; 379 G; 334 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1179;  DB 1;  Length 1512;
  Best Local Similarity   100.0%;  Pred. No. 0.00046;
  Matches 1179;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        269 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 328

Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 388

Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 448

Qy        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 508

Qy        241 ACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 ACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 568

Qy        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        569 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 628

Qy        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        629 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 688

Qy        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        689 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 748

Qy        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        749 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 808

Qy        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        809 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 868

Qy        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        869 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 928

Qy        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        929 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 988

Qy        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        989 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 1048

Qy        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1049 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 1108

Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db       1109 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 1168

Qy         901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1169 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 1228

Qy         961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1229 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1288

Qy        1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1289 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1348

Qy        1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1349 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1408

Qy        1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
               ||||||||||||||||||||||||||||||||||||||
Db        1409 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1447
```

RESULT 6
ADD93292

```
ID   ADD93292 standard; cDNA; 2061 BP.
XX
AC   ADD93292;
XX
DT   29-JAN-2004  (first entry)
XX
DE   p53-Chk1(1-270) fusion protein coding sequence.
XX
KW   ss; gene; p53-Chk1(1-270); fusion protein; modulation;
KW   serine/threonine kinase; phosphorylation; drug design; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2061
FT                   /*tag=  a
FT                   /product= "p53-Chk1(1-270)"
XX
PN   WO2003087394-A1.
XX
PD   23-OCT-2003.
XX
PF   15-APR-2003; 2003WO-EP003988.
XX
PR   15-APR-2002; 2002US-0372662P.
XX
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Suda M,  Shibahara M;
XX
DR   WPI; 2003-845339/78.
DR   P-PSDB; ADD93291.
DR   GENBANK; NM_001274.
XX
PT   Identifying a serine/threonine kinase modulator comprises expressing a
PT   substrate- serine/threonine kinase fusion protein in a cell, and
PT   determining phosphorylation level of the substrate in the presence of a
PT   candidate modulator.
XX
PS   Claim 7; Page 16; 38pp; English.
XX
CC   This sequence encodes a p53-Chk1(1-270) fusion protein. This sequence may
CC   be used in the method of the invention for identifying a modulator of a
CC   specific serine/threonine kinase. The method comprises expressing a
CC   fusion protein between a substrate and a serine/threonine kinase within a
CC   cell, and determining the level of phosphorylation of the substrate in
CC   the presence of a candidate modulator. The method is useful for screening
CC   modulators of serine/threonine kinases. Serine/threonine kinases are
```

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CC   useful as targets for drug design, e.g., in the treatment of cancer.
XX
SQ   Sequence 2061 BP; 552 A; 521 C; 531 G; 457 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1179;  DB 1;  Length 2061;
  Best Local Similarity 100.0%;  Pred. No. 0.00034;
  Matches 1179;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60

Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
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Db         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120

Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
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Db        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180

Qy        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
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Db        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360

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Qy        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
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Db        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540

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Qy        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
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Db        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720

Qy        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
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Db        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780

Qy        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
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Qy        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
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Db        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960

Qy        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020

Qy       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
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Db       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080

Qy       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140

Qy       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
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RESULT 7
ADD93290
ID   ADD93290 standard; cDNA; 2367 BP.
XX
AC   ADD93290;
XX
DT   29-JAN-2004  (first entry)
XX
DE   p53-SGK(60-431) fusion protein coding sequence.
XX
KW   ss; gene; p53-SGK(60-431); fusion protein; modulation;
KW   serine/threonine kinase; phosphorylation; drug design; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2367
FT                   /*tag= a
FT                   /product= "p53-SGK(60-431)"
XX
PN   WO2003087394-A1.
XX
PD   23-OCT-2003.
XX
PF   15-APR-2003; 2003WO-EP003988.
XX
PR   15-APR-2002; 2002US-0372662P.
XX
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Suda M,  Shibahara M;
XX
DR   WPI; 2003-845339/78.
DR   P-PSDB; ADD93289.
DR   GENBANK; XM_037046.
XX
PT   Identifying a serine/threonine kinase modulator comprises expressing a
PT   substrate- serine/threonine kinase fusion protein in a cell, and
PT   determining phosphorylation level of the substrate in the presence of a
PT   candidate modulator.
XX
PS   Claim 7; Page 15; 38pp; English.
XX
CC   This sequence encodes a p53-SGK(60-431) fusion protein. This sequence may
CC   be used in the method of the invention for identifying a modulator of a
CC   specific serine/threonine kinase. The method comprises expressing a
CC   fusion protein between a substrate and a serine/threonine kinase within a
CC   cell, and determining the level of phosphorylation of the substrate in
CC   the presence of a candidate modulator. The method is useful for screening
CC   modulators of serine/threonine kinases. Serine/threonine kinases are
CC   useful as targets for drug design, e.g., in the treatment of cancer.
XX
SQ   Sequence 2367 BP; 578 A; 672 C; 588 G; 529 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1179;  DB 1;  Length 2367;
  Best Local Similarity 100.0%;  Pred. No. 0.00029;
  Matches 1179;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60

Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
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Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
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Qy        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
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Qy        241 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
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Qy        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
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Db        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360

Qy        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420

Qy        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
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Qy        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
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Qy        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
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Db        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660

Qy        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720

Qy        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780

Qy        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840

Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900

Qy        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960

Qy        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020

Qy       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080

Qy       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
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Db       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140

Qy       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
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RESULT 8
ADD93288
ID ADD93288 standard; cDNA; 2385 BP.
XX
AC ADD93288;
XX
DT 29-JAN-2004 (first entry)
XX
DE p53-Myt1(1-378) fusion protein coding sequence.
XX
KW ss; gene; p53-Myt1(1-378); fusion protein; modulation;
KW serine/threonine kinase; phosphorylation; drug design; cancer.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .2385
FT   /*tag= a
FT   /product= "p53-Myt1(1-378)"
XX
PN WO2003087394-A1.
XX
PD 23-OCT-2003.
XX
PF 15-APR-2003; 2003WO-EP003988.
XX
PR 15-APR-2002; 2002US-0372662P.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Suda M, Shibahara M;
XX
DR WPI; 2003-845339/78.
DR P-PSDB; ADD93287.
DR GENBANK; U56816.
XX
PT Identifying a serine/threonine kinase modulator comprises expressing a
PT substrate- serine/threonine kinase fusion protein in a cell, and
PT determining phosphorylation level of the substrate in the presence of a
PT candidate modulator.
XX
PS Claim 7; Page 14; 38pp; English.
XX
CC This sequence encodes a p53-Myt1(1-378) fusion protein. This sequence may
CC be used in the method of the invention for identifying a modulator of a
CC specific serine/threonine kinase. The method comprises expressing a
CC fusion protein between a substrate and a serine/threonine kinase within a
CC cell, and determining the level of phosphorylation of the substrate in
CC the presence of a candidate modulator. The method is useful for screening
CC modulators of serine/threonine kinases. Serine/threonine kinases are
CC useful as targets for drug design, e.g., in the treatment of cancer.
XX
SQ Sequence 2385 BP; 466 A; 763 C; 720 G; 436 T; 0 U; 0 Other;

  Query Match   100.0%; Score 1179; DB 1; Length 2385;
  Best Local Similarity 100.0%; Pred. No. 0.00029;
  Matches 1179; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
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Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
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Qy       181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
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Qy       361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
Db       361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
Qy       421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
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Qy       481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
Db       481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
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Db       541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
Qy       601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
Db       601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
Qy       661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
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Qy       721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
Db       721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
Qy       781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
Db       781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
Qy       841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
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Qy       901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
Db       901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
Qy       961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
Db       961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
Qy      1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
Db      1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
Qy      1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
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Qy      1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
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RESULT 9
ADD93286
ID   ADD93286 standard; cDNA; 2406 BP.
XX
AC   ADD93286;
XX
DT   29-JAN-2004  (first entry)
XX
DE   p53-Yak3 fusion protein coding sequence.
XX
KW   ss; gene; p53-Yak3 ; fusion protein; modulation; serine/threonine kinase;
KW   phosphorylation; drug design; cancer.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2406
FT                   /*tag= a
FT                   /product= "p53-Yak3"
XX
PN   WO2003087394-A1.
XX
PD   23-OCT-2003.
XX
PF   15-APR-2003; 2003WO-EP003988.
XX
PR   15-APR-2002; 2002US-0372662P.
XX
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Suda M,  Shibahara M;
XX
DR   WPI; 2003-845339/78.
DR   P-PSDB; ADD93285.
DR   GENBANK; AF186773.
XX
PT   Identifying a serine/threonine kinase modulator comprises expressing a
PT   substrate- serine/threonine kinase fusion protein in a cell, and
PT   determining phosphorylation level of the substrate in the presence of a
PT   candidate modulator.
XX
PS   Claim 7; Page 13; 38pp; English.
XX
CC   This sequence encodes a p53-Yak3 fusion protein. This sequence may be
CC   used in the method of the invention for identifying a modulator of a
CC   specific serine/threonine kinase. The method comprises expressing a
CC   fusion protein between a substrate and a serine/threonine kinase within a
CC   cell, and determining the level of phosphorylation of the substrate in
CC   the presence of a candidate modulator. The method is useful for screening
CC   modulators of serine/threonine kinases. Serine/threonine kinases are
CC   useful as targets for drug design, e.g., in the treatment of cancer.
XX
SQ   Sequence 2406 BP; 611 A; 637 C; 622 G; 536 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1179;  DB 1;  Length 2406;
  Best Local Similarity  100.0%;  Pred. No. 0.00029;
  Matches 1179;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
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Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
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Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
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Qy        241 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
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Qy        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
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Qy        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420

Qy        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480

Qy        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540

Qy        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600

Qy        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660

Qy        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720

Qy        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780

Qy        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840

Db        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900

Qy        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960

Qy        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020

Qy       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080

Qy       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140

Qy       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
                 |||||||||||||||||||||||||||||||||||||||
Db       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179


RESULT 10
ADC35154
ID   ADC35154 standard; cDNA; 1182 BP.
XX
AC   ADC35154;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human breast cancer antigen polynucleotide seq id 38.
XX
KW   breast cancer; breast cancer diagnosis; breast cancer antigen; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2003108888-A1.
XX
PD   12-JUN-2003.
XX
PF   15-MAY-2002; 2002US-00146473.
XX
PR   15-MAY-2001; 2001US-0291150P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Scanlan MJ,  Gout I,  Stockert E,  Old LJ,  Gure A,  Chen Y;
XX
DR   WPI; 2003-829397/77.
DR   P-PSDB; ADC35112.
XX
PT   Diagnosing breast cancer in subject by obtaining biological sample from
PT   subject, contacting sample with breast cancer-associated polypeptides,
PT   determining specific binding between polypeptides and agents in sample.
XX
PS   Claim 1; SEQ ID NO 38; 173pp; English.
XX
CC   The invention describes a method of diagnosing breast cancer in subject
CC   comprising contacting biological sample from subject with at least two
CC   different breast cancer-associated polypeptides (I) encoded by nucleic
CC   acid molecules (II) comprising sequence chosen from 42 fully defined
CC   sequences as given in specification, determining specific binding between
CC   (I) and agents in sample, where presence of the binding is diagnostic for
CC   breast cancer. The method is useful for diagnosing breast cancer in a
CC   subject. The sample is blood, lymph node fluid or breast discharge fluid.
CC   This sequence encodes a breast cancer antigen.
XX
SQ   Sequence 1182 BP; 276 A; 364 C; 308 G; 234 T; 0 U; 0 Other;

  Query Match           99.9%;  Score 1177.4;  DB 1;  Length 1182;
  Best Local Similarity  99.9%;  Pred. No. 0.00059;
  Matches 1178;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGGAGCCGCAGTCAGATCCTAGCGTCGAGCCCCCTCTGAGTCAGGAAACATTTTCA 60

Qy         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACCTATGGAAACTACTTCCTGAAAACAACGTTCTGTCCCCCTTGCCGTCCCAAGCAATG 120

Qy        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GATGATTTGATGCTGTCCCCGGACGATATTGAACAATGGTTCACTGAAGACCCAGGTCCA 180

Qy        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGGACCAGCAGCTCCT 240

Qy        241 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACACCGGCGGCCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCCTTCCCAG 300

Qy        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTCTTGCATTCTGGGACAGCCAAG 360

Qy        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCTGTGACTTGCACGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACC 420
```

```
Qy        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCGGCACCCGCGTCCGCGCCATG 480

Qy        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCCCCCACCATGAG 540

Qy        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGCTGCTCAGATAGCGATGGTCTGGCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAAT 600

Qy        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACATAGTGTGGTGGTGCCCTAT 660

Qy        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGCCGCCTGAGGTTGGCTCTGACTGTACCACCATCCACTACAACTACATGTGTAACAGT 720

Qy        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TCCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCACCATCATCACACTGGAAGACTCC 780

Qy        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGA 840

Qy        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCC 900

Qy        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CCAGGGAGCACTAAGCGAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAG 960

Qy        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAACCACTGGATGGAGAATATTTCACCCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATG 1020

Qy       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTCCGAGAGCTGAATGAGGCCTTGGAACTCAAGGATGCCCAGGCTGGGAAGGAGCCAGGG 1080

Qy       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAAAAGGGTCAGTCTACCTCCCGCCAT 1140

Qy       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
              ||||||||||||||||||||||||||||||||||||||||
Db       1141 AAAAAACTCATGTTCAAGACAGAAGGGCCTGACTCAGAC 1179
```

RESULT 11
AAQ67884/c
ID AAQ67884 standard; DNA; 1182 BP.
XX
AC AAQ67884;
XX
DT 25-MAR-2003 (revised)
DT 23-MAR-1995 (first entry)
XX
DE Human p53 DNA.
XX
KW Polymerase chain reaction; primer; amplify; NYVAC; ALVAC; recombinant;
KW murine; interleukin-2; IL-2; pRW825; pmut-1; pBS-SK; pMM151; TK vector;
KW plasmid; vaccinia; H6 promoter; amplify; primer; antigenic response;
KW polymerase chain reaction; poxvirus; pSD542; immunological response;
KW pathogen; human; interferon; IFN; ss.
XX
OS Synthetic.
XX
PN WO9416716-A1.
XX
PD 04-AUG-1994.
XX
PF 21-JAN-1994; 94WO-US000888.
XX
PR 21-JAN-1993; 93US-00007115.
PR 19-JAN-1994; 94US-00184009.
XX
PA (VIRO-) VIROGENETICS CORP.
XX
PI Paoletti E, Tartaglia J, Cox WI;
XX
DR WPI; 1994-263767/32.
XX
PT Attenuated recombinant virus used for cancer therapy - comprises DNA
PT encoding cytokine and/or tumour associated antigen.
XX
PS Example 32; Fig 39; 232pp; English.
XX
CC This sequence represents the wildtype human p53 gene from the translation
CC initiation codon to the stop codon. This sequence was used in the
CC construction of an ALVAC-based recombinant virus containing a mutant form
CC of the human p53 gene. The mutant form has a G>A substitution at position
CC 524, changing an Arg residue at position 175 to a His residue. The
CC plasmid pMM110 (see also AAQ67864) contains the vaccinia H6 promoter and
CC the wild type human p53 gene in the ALVAC C5 insertion site. The mutant
CC p53 gene was obtained from plasmid Cx22A and cloned into pMM110 to
CC generate pMM143. Recombination between pMM143 and ALVAC rescuing virus
CC produced recombinant virus vCP270, which contains the vaccinia H6
CC promoted mutated human p53 in the C5 locus. The resulting virus may be
CC used in a composition for inducing an antigenic or immunological
CC response, ie. for immunisation against pathogens. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 1182 BP; 276 A; 365 C; 307 G; 234 T; 0 U; 0 Other;

Query Match 2.3%; Score 26.6; DB 1; Length 1182;
Best Local Similarity 51.2%; Pred. No. 12;
Matches 62; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

```
Qy        174 AGGTCCAGATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCCGCGTGGCCCCTGCACCAGC 233
              |||  |||| || |     |   |  | |||||| | |  | |  |||  || |  |||
Db        294 AGGGACAGAAGATGACAGGGGCCAGGAGGGGGCTGGTGCAGGGGCCGCCGGTGTAGGAGC 235

Qy        234 AGCTCCTACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCC 293
              |||  | ||  |||  | |  | | |||||  |    |    |       | || ||||  ||
Db        234 TGCTGGTGCAGGGGCCACGCGGGGAGCAGCCTCTGGCATTCTGGGAGCTTCATCTGGACC 175

Qy        294 T 294
              |
Db        174 T 174
```

RESULT 12
AAZ08529/c
ID AAZ08529 standard; DNA; 1182 BP.
XX
AC AAZ08529;
XX
DT 19-OCT-1999 (first entry)
XX
DE Human p53 gene.
XX
KW Attenuated recombinant virus; cytokine; tumour associated antigen;
KW NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rabies;
KW cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF;
KW interleukin; interferon; IFN-gamma; IL-4; melanoma associated antigen;
KW carcinoembryonic antigen; immunisation; antigenic; poxvirus; influenza;
KW immunological response; immunotherapy; vaccine; Newcastle Disease; ss.
XX
OS Homo sapiens.
XX

```
PN   US5942235-A.
XX
PD   24-AUG-1999.
XX
PF   02-JUN-1995;   95US-00458356.
XX
PR   24-DEC-1981;   81US-00334456.
PR   08-DEC-1982;   82US-00446824.
PR   19-JUN-1984;   84US-00622135.
PR   27-AUG-1987;   87US-00090209.
PR   28-AUG-1987;   87US-00090711.
PR   20-OCT-1987;   87US-00110335.
PR   25-APR-1988;   88US-00186054.
PR   23-AUG-1988;   88US-00234390.
PR   14-JUN-1990;   90US-00537882.
PR   14-JUN-1990;   90US-00537890.
PR   16-DEC-1991;   91US-00805567.
PR   03-MAR-1992;   92US-00847977.
PR   06-MAR-1992;   92US-00847951.
PR   04-MAY-1992;   92US-00881995.
PR   22-JUL-1992;   92US-00918278.
PR   20-JAN-1993;   93US-00007115.
PR   19-JAN-1994;   94US-00184009.
PR   14-APR-1994;   94US-00228926.
PR   13-SEP-1994;   94US-00306259.
XX
PA   (HEAL-) HEALTH RES INC.
XX
PI   Paoletti E;
XX
DR   WPI; 1999-493494/41.
XX
PT   Recombinant poxviruses comprising exogenous DNA encoding antigenic
PT   determinants useful in immunotherapy to immunize against cancers and
PT   other diseases such as influenza, Newcastle Disease and rabies.
XX
PS   Example 32; Fig 39; 163pp; English.
XX
CC   The present invention describes a recombinant poxvirus (I), comprising
CC   exogenous DNA encoding an antigenic determinant of a pathogen which is
CC   then expressed in vivo in infected host cells after administration to a
CC   patient and therefore induces an immunological response. (I) may be used
CC   to vaccinate patients against a wide range of diseases and disorders
CC   depending on the type of antigen encoded by the exogenous DNA. (I) may be
CC   used to vaccinate against diseases such as rabies, influenza and
CC   Newcastle Disease. It is particularly useful for immunising against
CC   cancers. The poxvirus (I) also provides a means of manipulating
CC   lymphocytes and tumour cells for use in cell-based immunotherapeutic
CC   modalities for cancer. (I) also have enhanced safety compared to
CC   unattenuated viruses (attenuation reduces the virulence of the viruses)
CC   and known recombinant poxvirus vaccines. This increased level of safety
CC   reduces the possibility of a 'runaway' infection in the host and reduces
CC   the chance of transmission from vaccinated to unvaccinated individuals
CC   and contamination of the environment. The present sequence represents a
CC   human p53 gene used in the exemplification of the present invention
XX
SQ   Sequence 1182 BP; 276 A; 365 C; 307 G; 234 T; 0 U; 0 Other;

  Query Match             2.3%;  Score 26.6;  DB 1;  Length 1182;
  Best Local Similarity   51.2%;  Pred. No. 12;
  Matches   62;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

Qy        174 AGGTCCAGATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGC 233
              |||  ||||  ||  |       |    |  |||||  |  |  |  |||  ||  |  |||
Db        294 AGGGACAGAAGATGACAGGGGCCAGGAGGGGGCTGGTGCAGGGGCCGCCGGTGTAGGAGC 235

Qy        234 AGCTCCTACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCC 293
               |||  |  ||  |||  |  |  |  |  ||||||  |    |    |       |||  ||||  ||
Db        234 TGCTGGTGCAGGGGCCACGCGGGGAGCAGCCTCTGGCATTCTGGGAGCTTCATCTGGACC 175

Qy        294 T 294
              |
Db        174 T 174
```

```
RESULT 13
AAH19387/c
ID   AAH19387 standard; cDNA; 1182 BP.
XX
AC   AAH19387;
XX
DT   03-AUG-2001  (first entry)
XX
DE   p53 coding sequence.
XX
KW   Cytostatic; gene therapy; p53; tumour; ss.
XX
OS   Unidentified.
XX
PN   JP2000354488-A.
XX
PD   26-DEC-2000.
XX
PF   09-APR-1999;   99JP-00139034.
XX
PR   09-APR-1999;   99JP-00139034.
XX
PA   (IKAW/) IKAWA H.
PA   (SAKA ) OTSUKA PHARM CO LTD.
XX
DR   WPI; 2001-268293/28.
DR   P-PSDB; AAB84836.
XX
PT   Chimera gene of the p53 family, useful for gene therapy, and treatment of
PT   cancer, comprises a transcription activating region and a DNA binding
PT   region.
XX
PS   Disclosure; Fig 2; 57pp; Japanese.
XX
CC   The present invention relates to a chimera gene of p53 family encoding a
CC   transcription activating region, a DNA binding region, and an oligomer
CC   formation region of different p53 family proteins. The chimeric gene can
CC   be used for gene therapy of p53 variant human tumours, and analysis of
CC   the function of the p53 family gene. The present sequence was used in the
CC   present invention
XX
SQ   Sequence 1182 BP; 276 A; 365 C; 307 G; 234 T; 0 U; 0 Other;

  Query Match             2.3%;  Score 26.6;  DB 1;  Length 1182;
  Best Local Similarity   51.2%;  Pred. No. 12;
  Matches   62;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

Qy        174 AGGTCCAGATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGC 233
              |||  ||||  ||  |       |    |  |||||  |  |  |  |||  ||  |  |||
Db        294 AGGGACAGAAGATGACAGGGGCCAGGAGGGGGCTGGTGCAGGGGCCGCCGGTGTAGGAGC 235

Qy        234 AGCTCCTACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCC 293
               |||  |  ||  |||  |  |  |  |  ||||||  |    |    |       |||  ||||  ||
Db        234 TGCTGGTGCAGGGGCCACGCGGGGAGCAGCCTCTGGCATTCTGGGAGCTTCATCTGGACC 175

Qy        294 T 294
              |
Db        174 T 174
```

```
RESULT 14
ADC35154/c
ID   ADC35154 standard; cDNA; 1182 BP.
XX
AC   ADC35154;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human breast cancer antigen polynucleotide seq id 38.
XX
KW   breast cancer; breast cancer diagnosis; breast cancer antigen; gene; ss.
```

XX
OS Homo sapiens.
XX
PN US2003108888-A1.
XX
PD 12-JUN-2003.
XX
PF 15-MAY-2002; 2002US-00146473.
XX
PR 15-MAY-2001; 2001US-0291150P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Scanlan MJ, Gout I, Stockert E, Old LJ, Gure A, Chen Y;
XX
DR WPI; 2003-829397/77.
DR P-PSDB; ADC35112.
XX
PT Diagnosing breast cancer in subject by obtaining biological sample from
PT subject, contacting sample with breast cancer-associated polypeptides,
PT determining specific binding between polypeptides and agents in sample.
XX
PS Claim 1; SEQ ID NO 38; 173pp; English.
XX
CC The invention describes a method of diagnosing breast cancer in subject
CC comprising contacting biological sample from subject with at least two
CC different breast cancer-associated polypeptides (I) encoded by nucleic
CC acid molecules (II) comprising sequence chosen from 42 fully defined
CC sequences as given in specification, determining specific binding between
CC (I) and agents in sample, where presence of the binding is diagnostic for
CC breast cancer. The method is useful for diagnosing breast cancer in a
CC subject. The sample is blood, lymph node fluid or breast discharge fluid.
CC This sequence encodes a breast cancer antigen.
XX
SQ Sequence 1182 BP; 276 A; 364 C; 308 G; 234 T; 0 U; 0 Other;

Query Match 2.3%; Score 26.6; DB 1; Length 1182;
Best Local Similarity 51.2%; Pred. No. 12;
Matches 62; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

```
Qy      174 AGGTCCAGATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGC 233
            ||| |||| || |      |   |  | |||||| | |  | |  |||  || |  |||
Db      294 AGGGACAGAAGATGACAGGGGCCAGGAGGGGGCTGGTGCAGGGGCCGCCGGTGTAGGAGC 235

Qy      234 AGCTCCTACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCC 293
            ||| | ||  ||| | |  | | ||||| |    |    |     | || ||||  ||
Db      234 TGCTGGTCCAGGGGCCACGCGGGGAGCAGCCTCTGGCATTCTGGGAGCTTCATCTGGACC 175

Qy      294 T 294
            |
Db      174 T 174
```

RESULT 15
AAZ08435/c
ID AAZ08435 standard; DNA; 1484 BP.
XX
AC AAZ08435;
XX
DT 19-OCT-1999 (first entry)
XX
DE H6/p53 (wildtype) expression cassette and flanking regions from vCP207.
XX
KW Attenuated recombinant virus; cytokine; tumour associated antigen;
KW NYVAC recombinant virus; ALVAC recombinant virus; gene therapy; rabies;
KW cancer; tumour necrosis factor; nuclear phosphoprotein; p53; IL-2; GMCSF;
KW interleukin; interferon; IFN-gamma; IL-4; melanoma associated antigen;
KW carcinoembryonic antigen; immunisation; antigenic; poxvirus; influenza;
KW immunological response; immunotherapy; vaccine; Newcastle Disease; ss.
XX
OS Synthetic.
OS Homo sapiens.
OS Vaccinia virus.

XX
PN US5942235-A.
XX
PD 24-AUG-1999.
XX
PF 02-JUN-1995; 95US-00458356.
XX
PR 24-DEC-1981; 81US-00334456.
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XX
PA (HEAL-) HEALTH RES INC.
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PI Paoletti E;
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DR WPI; 1999-493494/41.
XX
PT Recombinant poxviruses comprising exogenous DNA encoding antigenic
PT determinants useful in immunotherapy to immunize against cancers and
PT other diseases such as influenza, Newcastle Disease and rabies.
XX
PS Example 15; Fig 18; 163pp; English.
XX
CC The present invention describes a recombinant poxvirus (I), comprising
CC exogenous DNA encoding an antigenic determinant of a pathogen which is
CC then expressed in vivo in infected host cells after administration to a
CC patient and therefore induces an immunological response. (I) may be used
CC to vaccinate patients against a wide range of diseases and disorders
CC depending on the type of antigen encoded by the exogenous DNA. (I) may be
CC used to vaccinate against diseases such as rabies, influenza and
CC Newcastle Disease. It is particularly useful for immunising against
CC cancers. The poxvirus (I) also provides a means of manipulating
CC lymphocytes and tumour cells for use in cell-based immunotherapeutic
CC modalities for cancer. (I) also have enhanced safety compared to
CC unattenuated viruses (attenuation reduces the virulence of the viruses)
CC and known recombinant poxvirus vaccines. This increased level of safety
CC reduces the possibility of a 'runaway' infection in the host and reduces
CC the chance of transmission from vaccinated to unvaccinated individuals
CC and contamination of the environment. The present sequence represents a
CC H6/p53 (wildtype) expression cassette and flanking regions from vCP207
CC used in the exemplification of the present invention
XX
SQ Sequence 1484 BP; 367 A; 416 C; 371 G; 330 T; 0 U; 0 Other;

Query Match 2.3%; Score 26.6; DB 1; Length 1484;
Best Local Similarity 51.2%; Pred. No. 9.9;
Matches 62; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

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Qy      174 AGGTCCAGATGAAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGC 233
            ||| |||| || |      |   |  | |||||| | |  | |  |||  || |  |||
Db      526 AGGGACAGAAGATGACAGGGGCCAGGAGGGGGCTGGTGCAGGGGCCGCCGGTGTAGGAGC 467

Qy      234 AGCTCCTACACCGGCGGCCCCTGCACCAGCCCCCTCCTGGCCCCTGTCATCTTCTGTCCC 293
            ||| | ||  ||| | |  | | ||||| |    |    |     | || ||||  ||
Db      466 TGCTGGTGCAGGGGCCACGCGGGGAGCAGCCTCTGGCATTCTGGGAGCTTCATCTGGACC 407

Qy      294 T 294
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Db 406 T 406

Search completed: September 28, 2004, 12:07:34
Job time : 18 secs